SEQUENCE LISTING

<110> Saris, Chris

<120> ISOLATION, IDENTIFICATION, AND CHARACTERIZATION OF TMST2, A NOVEL MEMBER OF THE TNF-RECEPTOR SUPERFAMILY OF GENES

<130> 01017/35434B

<140> To be assigned
<141> Herewith

<150> US 09/612,033
<151> 2000-07-07

<150> US 60/143,063
<151> 1999-07-09

<160> 15

<170> PatentIn Ver. 2.0

<210> 1
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<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic primer

<220>
<221> misc_feature
<222> (25)..(33)
<223> N = A or T or G or C

<220>
<223> Primer 1360-38

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ggaaggaaaa aagcggccgc aacannnnnn nnn 33

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<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic primer

<220>
<223> Primer 1605-21

<400> 2
aatccgatgc ccacgttgca gta 23

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<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic primer

<220>
<223> Primer 1239-08

<400> 3
aaaatcttag accgacgact gtgttt 26

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<212> DNA
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<220>
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<220>
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<400> 4
gagtctccgc agccttttga gg 22

<210> 5
<211> 412
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (13)..(411)

<220>
<223> tmst2 00004-d1

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ttgcactcgg cc atg ttt ggc ttc ttc tgc agc ttg gtg tcc agt ctg agt 51
Met Phe Gly Phe Phe Cys Ser Leu Val Ser Ser Leu Ser
1 5 10

cgc tgg ttc ctt tgg cgg cgg ctg ctg ctg ctg ctg ctg ctg ctg ctg 99
Arg Trp Phe Leu Trp Arg Arg Leu Leu Leu Leu Leu Leu Leu Leu Leu
15 20 25

ctg aat ctg ccc ttg cag gta aaa ttt gct atg cta gaa tta cac tcc 147
Leu Asn Leu Pro Leu Gln Val Lys Phe Ala Met Leu Glu Leu His Ser
30 35 40 45

ttc aaa tgt ccc gct ggt gaa tac tgg tct aaa gac gtc tgt tgc aag 195
Phe Lys Cys Pro Ala Gly Glu Tyr Trp Ser Lys Asp Val Cys Cys Lys
50 55 60

aac tgt tct gca ggt aca ttt gtc aag gcg ccc tgc gaa atc ccc cat 243
Asn Cys Ser Ala Gly Thr Phe Val Lys Ala Pro Cys Glu Ile Pro His
65 70 75

act caa gga caa tgt gag aag tgt cac cca gga aca ttc aca gag aaa 291
Thr Gln Gly Gln Cys Glu Lys Cys His Pro Gly Thr Phe Thr Glu Lys
80 85 90

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gat aat tac ctg gat gct tgt ata ctt tgc tcc acc tgt gat aaa gat   339
Asp Asn Tyr Leu Asp Ala Cys Ile Leu Cys Ser Thr Cys Asp Lys Asp
     95                  100                 105

cag gaa atg gtg gcc gac tgc tca gcc acc agt gac cgg aaa tgc cag   387
Gln Glu Met Val Ala Asp Cys Ser Ala Thr Ser Asp Arg Lys Cys Gln
110                 115                 120                 125

tgc cga aca ggt ctt tac tac tat g                                412
Cys Arg Thr Gly Leu Tyr Tyr Tyr
                130
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<210> 6
<211> 133
<212> PRT
<213> Mus musculus

<400> 6

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Leu Trp Arg Arg Leu Leu Leu Leu Leu Leu Leu Leu Leu Leu Asn Leu
            20                  25                  30

Pro Leu Gln Val Lys Phe Ala Met Leu Glu Leu His Ser Phe Lys Cys
        35                  40                  45

Pro Ala Gly Glu Tyr Trp Ser Lys Asp Val Cys Cys Lys Asn Cys Ser
     50                  55                  60

Ala Gly Thr Phe Val Lys Ala Pro Cys Glu Ile Pro His Thr Gln Gly
 65                  70                  75                  80

Gln Cys Glu Lys Cys His Pro Gly Thr Phe Thr Glu Lys Asp Asn Tyr
                85                  90                  95

Leu Asp Ala Cys Ile Leu Cys Ser Thr Cys Asp Lys Asp Gln Glu Met
            100                 105                 110

Val Ala Asp Cys Ser Ala Thr Ser Asp Arg Lys Cys Gln Cys Arg Thr
        115                 120                 125

Gly Leu Tyr Tyr Tyr
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<210> 7
<211> 1550
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (13)..(606)

<220>
<223> mouse tmst2

<400> 7

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              Met Phe Gly Phe Phe Cys Ser Leu Val Ser Ser Leu Ser
                1               5                  10
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cgc tgg ttc ctt tgg cgg cgg ctg ctg ctg ctg ctg ctg ctg ctg ctg   99
Arg Trp Phe Leu Trp Arg Arg Leu Leu Leu Leu Leu Leu Leu Leu Leu
     15                  20                  25

ctg aat ctg ccc ttg cag gta aaa ttt gct atg cta gaa tta cac tcc   147
Leu Asn Leu Pro Leu Gln Val Lys Phe Ala Met Leu Glu Leu His Ser
 30                  35                  40                  45

ttc aaa tgt ccc gct ggt gaa tac tgg tct aaa gac gtc tgt tgc aag   195
Phe Lys Cys Pro Ala Gly Glu Tyr Trp Ser Lys Asp Val Cys Cys Lys
                 50                  55                  60

aac tgt tct gca ggt aca ttt gtc aag gcg ccc tgc gaa atc ccc cat   243
Asn Cys Ser Ala Gly Thr Phe Val Lys Ala Pro Cys Glu Ile Pro His
             65                  70                  75

act caa gga caa tgt gag aag tgt cac cca gga aca ttc aca gag aaa   291
Thr Gln Gly Gln Cys Glu Lys Cys His Pro Gly Thr Phe Thr Glu Lys
         80                  85                  90

gat aat tac ctg gat gct tgt ata ctt tgc tcc acc tgt gat aaa gat   339
Asp Asn Tyr Leu Asp Ala Cys Ile Leu Cys Ser Thr Cys Asp Lys Asp
     95                 100                 105

cag gaa atg gtg gcc gac tgc tca gcc acc agt gac cgg aaa tgc cag   387
Gln Glu Met Val Ala Asp Cys Ser Ala Thr Ser Asp Arg Lys Cys Gln
110                 115                 120                 125

tgc cga aca ggt ctt tac tac tat gac cca aaa ttt cca gaa tcg tgc   435
Cys Arg Thr Gly Leu Tyr Tyr Tyr Asp Pro Lys Phe Pro Glu Ser Cys
                130                 135                 140

cgc cca tgt acc aag tgt ccc caa gga atc cct gtc ctc cag gaa tgc   483
Arg Pro Cys Thr Lys Cys Pro Gln Gly Ile Pro Val Leu Gln Glu Cys
            145                 150                 155

aac tcc aca gct aac act gtg tgc agt tca tct gtt tca aat ccc aga   531
Asn Ser Thr Ala Asn Thr Val Cys Ser Ser Ser Val Ser Asn Pro Arg
        160                 165                 170

aac cgg ctg ttc cta ctg tta tca cct ttg agt gtg cta att gtg tcc   579
Asn Arg Leu Phe Leu Leu Leu Ser Pro Leu Ser Val Leu Ile Val Ser
    175                 180                 185

gtt gtt gtc ttc cgt atc ata aga aga taaaggttct acagatgttt         626
Val Val Val Phe Arg Ile Ile Arg Arg
190                 195

tcttagcttc cttttattgc tatgaagtga tactatggag gcaactcttt tattttattt 686

attttatttt atttttaat gtcttgaact tgatttgaag accaggctgg cctcaaaatc 746

acagagatcc agactaagac aactctaata agggaaacat ttaattggga ctggcttaca 806

gtttcggacg ttttgtccat gattatcata gtgggaagca tggcagcatc taagcagaca 866

tgatgttgga gaaggagctg agatttctgc atcttgatct gcaagcaata aaaggagact 926

gtgtgccaca ctatacacag cttgaacata ggagacctca aagcctgtcc ccacagtgac 986

aaacttcctc caacaaggtc atacctccta ataataccat ttcttatgag gcaagcattc 1046

aaacacatga gtctatgagg gccaaaccaa ttcaaaccac cacaggttaa caattgccct 1106
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ctgcagctct ctggtggagg ccctccttga gagtaagtaa caatttagat gaaggcaagt 1166

cctggtatca ggtccaaaag aaactcagga tgaatggtcc actgtggttc ctattaacat 1226

actgaagaac atgacctcac cttacacgtc tccacctcac tgacttccct tcccctagct 1286

tctcattccc aggtaaccct gccatttttt ggtaatgtgc cttcttggtt cttcctctcc 1346

tttccccctc tcttctggtc cttacttctc ttcctctccc actctccacc agcctcctct 1406

taaggcctga atcagtctgt aggtcatgtt taatctacta ctttctctct gctctggact 1466

catccagatg tctctggctg agctctccct cctatctaca ataaaaccct tcccccctaac 1526

cagaaatgca aaaaaaaaaa aaaa 1550

<210> 8
<211> 198
<212> PRT
<213> Mus musculus

<400> 8

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Leu	Trp	Arg	Arg	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Asn	Leu	
			20					25					30			
Pro	Leu	Gln	Val	Lys	Phe	Ala	Met	Leu	Glu	Leu	His	Ser	Phe	Lys	Cys	
		35					40					45				
Pro	Ala	Gly	Glu	Tyr	Trp	Ser	Lys	Asp	Val	Cys	Cys	Lys	Asn	Cys	Ser	
	50					55					60					
Ala	Gly	Thr	Phe	Val	Lys	Ala	Pro	Cys	Glu	Ile	Pro	His	Thr	Gln	Gly	
65					70					75						80
Gln	Cys	Glu	Lys	Cys	His	Pro	Gly	Thr	Phe	Thr	Glu	Lys	Asp	Asn	Tyr	
				85					90					95		
Leu	Asp	Ala	Cys	Ile	Leu	Cys	Ser	Thr	Cys	Asp	Lys	Asp	Gln	Glu	Met	
			100					105					110			
Val	Ala	Asp	Cys	Ser	Ala	Thr	Ser	Asp	Arg	Lys	Cys	Gln	Cys	Arg	Thr	
		115					120					125				
Gly	Leu	Tyr	Tyr	Tyr	Asp	Pro	Lys	Phe	Pro	Glu	Ser	Cys	Arg	Pro	Cys	
	130					135					140					
Thr	Lys	Cys	Pro	Gln	Gly	Ile	Pro	Val	Leu	Gln	Glu	Cys	Asn	Ser	Thr	
145					150					155						160
Ala	Asn	Thr	Val	Cys	Ser	Ser	Ser	Val	Ser	Asn	Pro	Arg	Asn	Arg	Leu	
				165					170					175		
Phe	Leu	Leu	Leu	Ser	Pro	Leu	Ser	Val	Leu	Ile	Val	Ser	Val	Val	Val	
			180					185					190			
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<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (13)..(552)

<220>
<223> Primer 2086-39

<400> 9

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                1               5                  10

cgc tgg ttc ctt tgg cgg cgg ctg ctg ctg ctg ctg ctg ctg ctg ctg   99
Arg Trp Phe Leu Trp Arg Arg Leu Leu Leu Leu Leu Leu Leu Leu Leu
     15                  20                  25

ctg aat ctg ccc ttg cag gta aaa ttt gct atg cta gaa tta cac tcc   147
Leu Asn Leu Pro Leu Gln Val Lys Phe Ala Met Leu Glu Leu His Ser
 30                  35                  40                  45

ttc aaa tgt ccc gct ggt gaa tac tgg tct aaa gac gtc tgt tgc aag   195
Phe Lys Cys Pro Ala Gly Glu Tyr Trp Ser Lys Asp Val Cys Cys Lys
                 50                  55                  60

aac tgt tct gca ggt aca ttt gtc aag gcg ccc tgc gaa atc ccc cat   243
Asn Cys Ser Ala Gly Thr Phe Val Lys Ala Pro Cys Glu Ile Pro His
             65                  70                  75

act caa gga caa tgt gag aag tgt cac cca gga aca ttc aca gag aaa   291
Thr Gln Gly Gln Cys Glu Lys Cys His Pro Gly Thr Phe Thr Glu Lys
         80                  85                  90

gat aat tac ctg gat gct tgt ata ctt tgc tcc acc tgt gat aaa gat   339
Asp Asn Tyr Leu Asp Ala Cys Ile Leu Cys Ser Thr Cys Asp Lys Asp
     95                  100                 105

cag gaa atg gtg gcc gac tgc tca gcc acc agt gac cgg aaa tgc cag   387
Gln Glu Met Val Ala Asp Cys Ser Ala Thr Ser Asp Arg Lys Cys Gln
110                 115                 120                 125

tgc cga aca ggt ctt tac tac tat gac cca aaa ttt cca gaa tcg tgc   435
Cys Arg Thr Gly Leu Tyr Tyr Tyr Asp Pro Lys Phe Pro Glu Ser Cys
                130                 135                 140

cgc cca tgt acc aag tgt ccc caa gga atc cct gtc ctc cag gaa tgc   483
Arg Pro Cys Thr Lys Cys Pro Gln Gly Ile Pro Val Leu Gln Glu Cys
            145                 150                 155

aac tcc aca gct aac act gtg tgc agt tca tct gtt tca aga aga tct   531
Asn Ser Thr Ala Asn Thr Val Cys Ser Ser Ser Val Ser Arg Arg Ser
        160                 165                 170

gcc tca gtg gcc tgg cct atc tgaatggttc acagagatcc cagaaaccgg      582
Ala Ser Val Ala Trp Pro Ile
    175                 180
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ctgttcctac tgttatcacc tttgagtgtg ctaattgtgt ccgttgttgt cttccgtatc 642

ataagaagat aaaggttcta cagatgtttt cttagcttcc ttttattgct atgaagtgat 702

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<212> PRT
<213> Mus musculus

<400> 10

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  1               5                  10                  15

Leu Trp Arg Arg Leu Leu Leu Leu Leu Leu Leu Leu Leu Leu Asn Leu
             20                  25                  30

Pro Leu Gln Val Lys Phe Ala Met Leu Glu Leu His Ser Phe Lys Cys
         35                  40                  45

Pro Ala Gly Glu Tyr Trp Ser Lys Asp Val Cys Cys Lys Asn Cys Ser
     50                  55                  60

Ala Gly Thr Phe Val Lys Ala Pro Cys Glu Ile Pro His Thr Gln Gly
 65                  70                  75                  80

Gln Cys Glu Lys Cys His Pro Gly Thr Phe Thr Glu Lys Asp Asn Tyr
                 85                  90                  95

Leu Asp Ala Cys Ile Leu Cys Ser Thr Cys Asp Lys Asp Gln Glu Met
            100                 105                 110

Val Ala Asp Cys Ser Ala Thr Ser Asp Arg Lys Cys Gln Cys Arg Thr
        115                 120                 125

Gly Leu Tyr Tyr Tyr Asp Pro Lys Phe Pro Glu Ser Cys Arg Pro Cys
    130                 135                 140

Thr Lys Cys Pro Gln Gly Ile Pro Val Leu Gln Glu Cys Asn Ser Thr
145                 150                 155                 160

Ala Asn Thr Val Cys Ser Ser Ser Val Ser Arg Arg Ser Ala Ser Val
                165                 170                 175

Ala Trp Pro Ile
            180
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<210> 11
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic primer

<220>
<223> Primer 2038-41

<400> 11
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<210> 12
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic primer

<220>
<223> tmst2-Ig fusion protein

<400> 12
ttgtcgacat ttgaaacaga tgaactgcac aca 33

<210> 13
<211> 1200
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Fusion protein
consisting of Mus musculus sequences and
Immunoglobulin sequences

<220>
<221> CDS
<222> (1)..(1194)

<400> 13
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1 5 10 15

ctt tgg cgg cgg ctg ctg ctg ctg ctg ctg ctg ctg ctg ctg aat ctg 96
Leu Trp Arg Arg Leu Leu Leu Leu Leu Leu Leu Leu Leu Asn Leu
20 25 30

ccc ttg cag gta aaa ttt gct atg cta gaa tta cac tcc ttc aaa tgt 144
Pro Leu Gln Val Lys Phe Ala Met Leu Glu Leu His Ser Phe Lys Cys
35 40 45

ccc gct ggt gaa tac tgg tct aaa gac gtc tgt tgc aag aac tgt tct 192
Pro Ala Gly Glu Tyr Trp Ser Lys Asp Val Cys Cys Lys Asn Cys Ser
50 55 60

gca ggt aca ttt gtc aag gcg ccc tgc gaa atc ccc cat act caa gga 240
Ala Gly Thr Phe Val Lys Ala Pro Cys Glu Ile Pro His Thr Gln Gly
65 70 75 80

caa tgt gag aag tgt cac cca gga aca ttc aca gag aaa gat aat tac 288
Gln Cys Glu Lys Cys His Pro Gly Thr Phe Thr Glu Lys Asp Asn Tyr
85 90 95

ctg gat gct tgt ata ctt tgc tcc acc tgt gat aaa gat cag gaa atg 336
Leu Asp Ala Cys Ile Leu Cys Ser Thr Cys Asp Lys Asp Gln Glu Met
100 105 110

gtg gcc gac tgc tca gcc acc agt gac cgg aaa tgc cag tgc cga aca 384
Val Ala Asp Cys Ser Ala Thr Ser Asp Arg Lys Cys Gln Cys Arg Thr
115 120 125

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ggt ctt tac tac tat gac cca aaa ttt cca gaa tcg tgc cgc cca tgt   432
Gly Leu Tyr Tyr Tyr Asp Pro Lys Phe Pro Glu Ser Cys Arg Pro Cys
    130                 135                 140

acc aag tgt ccc caa gga atc cct gtc ctc cag gaa tgc aac tcc aca   480
Thr Lys Cys Pro Gln Gly Ile Pro Val Leu Gln Glu Cys Asn Ser Thr
145                 150                 155                 160

gct aac act gtg tgc agt tca tct gtt tca aat gtc gac act cac aca   528
Ala Asn Thr Val Cys Ser Ser Ser Val Ser Asn Val Asp Thr His Thr
                165                 170                 175

tgc cca ccg tgc cca gca cct gaa ctc ctg ggg gga ccg tca gtc ttc   576
Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe
            180                 185                 190

ctc ttc ccc cca aaa ccc aag gac acc ctc atg atc tcc cgg acc cct   624
Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
        195                 200                 205

gag gtc aca tgc gtg gtg gtg gac gtg agc cac gaa gac cct gag gtc   672
Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
    210                 215                 220

aag ttc aac tgg tac gtg gac ggc gtg gag gtg cat aat gcc aag aca   720
Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
225                 230                 235                 240

aag ccg cgg gag gag cag tac aac agc acg tac cgt gtg gtc agc gtc   768
Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
                245                 250                 255

ctc acc gtc ctg cac cag gac tgg ctg aat ggc aag gag tac aag tgc   816
Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
            260                 265                 270

aag gtc tcc aac aaa gcc ctc cca gcc ccc atc gag aaa acc atc tcc   864
Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
        275                 280                 285

aaa gcc aaa ggg cag ccc cga gaa cca cag gtg tac acc ctg ccc cca   912
Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
    290                 295                 300

tcc cgg gat gag ctg acc aag aac cag gtc agc ctg acc tgc ctg gtc   960
Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
305                 310                 315                 320

aaa ggc ttc tat ccc agc gac atc gcc gtg gag tgg gag agc aat ggg  1008
Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
                325                 330                 335

cag ccg gag aac aac tac aag acc acg cct ccc gtg ctg gac tcc gac  1056
Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
            340                 345                 350

ggc tcc ttc ttc ctc tac agc aag ctc acc gtg gac aag agc agg tgg  1104
Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
        355                 360                 365
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cag cag ggg aac gtc ttc tca tgc tcc gtg atg cat gag gct ctg cac   1152
Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
    370                 375                 380

aac cac tac acg cag aag agc ctc tcc ctg tct ccg ggt aaa tgataa    1200
Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
385                 390                 395
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<210> 14
<211> 398
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Fusion protein consisting of Mus musculus sequences and Immunoglobulin sequences

<400> 14

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Met Phe Gly Phe Phe Cys Ser Leu Val Ser Ser Leu Ser Arg Trp Phe
  1               5                  10                  15

Leu Trp Arg Arg Leu Leu Leu Leu Leu Leu Leu Leu Leu Leu Asn Leu
            20                  25                  30

Pro Leu Gln Val Lys Phe Ala Met Leu Glu Leu His Ser Phe Lys Cys
        35                  40                  45

Pro Ala Gly Glu Tyr Trp Ser Lys Asp Val Cys Cys Lys Asn Cys Ser
    50                  55                  60

Ala Gly Thr Phe Val Lys Ala Pro Cys Glu Ile Pro His Thr Gln Gly
65                  70                  75                  80

Gln Cys Glu Lys Cys His Pro Gly Thr Phe Thr Glu Lys Asp Asn Tyr
                85                  90                  95


Leu Asp Ala Cys Ile Leu Cys Ser Thr Cys Asp Lys Asp Gln Glu Met
            100                 105                 110

Val Ala Asp Cys Ser Ala Thr Ser Asp Arg Lys Cys Gln Cys Arg Thr
        115                 120                 125

Gly Leu Tyr Tyr Tyr Asp Pro Lys Phe Pro Glu Ser Cys Arg Pro Cys
    130                 135                 140

Thr Lys Cys Pro Gln Gly Ile Pro Val Leu Gln Glu Cys Asn Ser Thr
145                 150                 155                 160

Ala Asn Thr Val Cys Ser Ser Ser Val Ser Asn Val Asp Thr His Thr
                165                 170                 175

Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe
            180                 185                 190

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
        195                 200                 205

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
    210                 215                 220
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Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
225                 230                 235                 240

Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
                245                 250                 255

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
            260                 265                 270

Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
        275                 280                 285

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
    290                 295                 300

Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
305                 310                 315                 320

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
                325                 330                 335

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
            340                 345                 350

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
        355                 360                 365

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
    370                 375                 380

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
385                 390                 395
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<210> 15
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Systhetic peptide

<400> 15

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Tyr Gly Arg Lys Lys Arg Arg Gln Arg Arg Arg
  1               5                  10
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